# Single-Cell and Spatial Omics: Methods and Applications

**Date: December 5-6, 2024**
**Organized by:**
Prof. Can Yang, Department of Mathematics, HKUST
Prof. Jiguang Wang, Division of Life Science, HKUST
**Location:**
Room 2502, Lift 25-26

## Day 1, 05/12/2024

| Time | Schedule |
|---|---|
| 14:00-15:20 | **Workshop:**<br>**Unlocking single-cell spatial omics analyses with SCDNEY**<br>*Mentor: Jean Yang*<br>*Instructors: Yue Cao, Daniel Kim* |
| 15:20-15:40 | Tea break |
| 15:40-17:00 | **Workshop:**<br>**Unlocking single-cell spatial omics analyses with SCDNEY**<br>*Mentor: Jean Yang*<br>*Instructors: Yue Cao, Daniel Kim* |
| 18:00-20:00 | **Dinner (by invitation only)** |

## Day 2, 06/12/2024

| Time | Schedule |
|---|---|
| 9:00-9:05 | Taking Group photos |
| 9:05-9:40 | **Positive selection in normal and precancerous tissues**<br>*POON, Gladys Yeuk Pin, The University of Hong Kong* |
| 9:40-10:15 | **Analysis of transcript variants from single-cell and spatial RNA-seq data**<br>*Yuanhua Huang, The University of Hong Kong* |
| 10:15-10:50 | **Single-cell analyses reveal the PVR/TIGIT axis-mediated immune evasion in IDH-wildtype glioblastoma**<br>*Zheng Zhao, Beijing Neurosurgical Institute, Beijing Tiantan Hospital* |
| 10:50-11:05 | Tea Break |
| 11:05-11:40 | **Integrative Analysis and Regulatory Inference in Spatial Multi-Omics Data via Graph Representation Learning** |

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| | *Zhixiang Lin, The Chinese University of Hong Kong* |
| 12:00-14:00 | **Lunch (by invitation only)** |

**Dr. Jean Yang (Thursday, 14:00-17:00)**

Bio: Jean Yang is a Professor at the School of Mathematics and Statistics at the University of Sydney. Her research stands at the interface between medicine and methodology development and has centred on the development of methods and the application of statistics to problems in omics and biomedical research.

**Dr. Yue Cao (Thursday, 14:00-17:00)**

**Bio:** Yue Cao is a post-doctoral researcher at the School of Mathematics and Statistics at the University of Sydney. Her research focus is on computational analysis of high-dimensional omics data, particularly single-cell multi-omics data for precision medicine.

**Mr. Daniel Kim (Thursday, 14:00-17:00)**

**Bio:** Daniel is in his final year of his PhD at the Faculty of Medicine and Health at the University of Sydney, developing computational methods for analyzing high-dimensional omics data. He is also completing a Masters degree in applied statistics at the University of Macquarie and is passionate about learning statistics, biology, and teaching.

**Title: Unlocking single-cell spatial omics analyses with SCDNEY**

**Abstract:**

The workshop will begin with an introductory presentation on spatial omics technologies, and associated analyses. We will then explore the challenges and analytical focus associated with predicting outcomes using multi-condition and – sample spatial data. The workshop will illustrate general analytic strategies to address commonly asked questions such as how to predict patient outcomes. We will also discuss critical thinking questions that commonly arise. The workshop will cover the following:

● Extracting informative scRNA-seq and spatial features via scFeatures.
● Strategies for building classification models using machine learning techniques via ClassifyR.
● Understanding transformation from cell level to patient level features.
● Identification of cohort heterogeneity and its implications.

**Dr. POON, Gladys Yeuk Pin (Friday, 9:05-9:40)**

**Bio:** Gladys is a research assistant professor at the School of Biomedical Sciences, Li Ka Shing Faculty of Medicine at HKU. She completed her undergraduate studies in physics at the University of Cambridge, followed by a PhD in Oncology. With the unique combination of expertise in both quantitative thinking and biological understanding, her research bridges cancer genomics, evolutionary biology and mathematical modelling with experiments. Her work has advanced understanding in the somatic evolution of normal and precancerous human tissues.

**Title: Positive selection in normal and precancerous tissues**


**Dr. Yuanhua Huang (Friday, 9:40-10:15)**
**Bio:** Dr. Huang is an assistant professor in the School of Biomedical Sciences and the Department of Statistics and Actuarial Science at the University of Hong Kong (HKU). Prior to joining HKU, he was an EBPOD research fellow at the University of Cambridge and the European Bioinformatics Institute (EMBL-EBI). Dr Huang completed his BEng in Automation from Tsinghua University (2013) and PhD in Informatics from the University of Edinburgh (2017). His lab works at the interface between data science and genomics and is supported by the NSFC Excellent Young Scientist fund for single-cell data science.

**Title: Analysis of transcript variants from single-cell and spatial RNA-seq data**


**Dr. Zheng Zhao (Friday, 10:15-10:50)**
**Bio:** Zheng Zhao serves as an associate professor at the Beijing Neurosurgical Institute, where he focuses on establishing molecular classifications for gliomas, developing biomedical databases, and investigating the immune microenvironment and heterogeneity of gliomas. He has published 29 papers in SCI journals, including Cancer Discovery, Molecular Cancer, and Cell Reports Medicine. Currently, he is the lead executor of the Chinese Glioma Genome Atlas (CGGA) Project and Chinese Neuro-Oncology Genome Atlas (CGGA-CNS) Project

**Title: Single-cell analyses reveal the PVR/TIGIT axis-mediated immune evasion in IDH-wildtype glioblastoma**


**Dr. Zhixiang Lin (Friday, 11:05-11:40)**
**Bio:** Zhixiang Lin is currently an associate professor in the Department of Statistics at the Chinese University of Hong Kong. His research focuses on developing novel statistical methods and computational tools for addressing significant scientific questions, especially those related to the analysis and interpretation of large-scale

genomic data.

**Title: Integrative Analysis and Regulatory Inference in Spatial Multi-Omics Data via Graph Representation Learning**